



PCT/99

RAW SEQUENCE LISTING

DATE: 05/21/2002

PATENT APPLICATION: US/09/807,721

TIME: 15:54:10

Input Set : A:\PTO.VSK.txt

Output Set: N:\CRF3\05212002\I807721.raw

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3 <110> APPLICANT: AUBURN UNIVERSITY
4   UNIVERSITY OF CENTRAL FLORIDA
6 <120> TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
8 <130> FILE REFERENCE: 1463-PCT-US-00
10 <140> CURRENT APPLICATION NUMBER: 09/807,721
C--> 11 <141> CURRENT FILING DATE: 2001-12-21
13 <150> PRIOR APPLICATION NUMBER: PCT/US01/06274
14 <151> PRIOR FILING DATE: 2001-02-28
16 <160> NUMBER OF SEQ ID NOS: 6
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2059
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
25 <220> FEATURE:
26 <221> NAME/KEY: CDS
27 <222> LOCATION: (17..1381, 1409..2050)
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31           Met Gly Val Gln Leu Gln Gln Ser Gly Pro Asp
32           1               5               10
34 ctg gtg aaa cct ggg gcc tca gtg aag ata tcc tgc aag gct tct gga      97
35 Leu Val Lys Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly
36           15               20               25
38 tac aca ttc act gac tac aac ata cac tgg gtg aag cag agc cgt gga      145
39 Tyr Thr Phe Thr Asp Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly
40           30               35               40
42 aag agc ctt gag tgg att gga tat att tat cct tac aat ggt aat act      193
43 Lys Ser Leu Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr
44           45               50               55
46 tac tac aac cag aag ttc aag aac aag gcc aca ttg act gta gac aat      241
47 Tyr Tyr Asn Gln Lys Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn
48 60           65               70               75
50 tcc tcc acc tca gcc tac atg gag ctc cgc agc ctg aca tct gag gac      289
51 Ser Ser Thr Ser Ala Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp
52           80               85               90
54 tct gca gtc tat tac tgt gca acc tac ttt gac tac tgg ggc caa ggc      337
55 Ser Ala Val Tyr Tyr Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly
56           95               100              105
58 acc act ctc aca gtg agc tca gca tcc ccg acc agc ccc aag gtc ttc      385
59 Thr Thr Leu Thr Val Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe
60           110              115              120
62 ccg ctg agc ctc gac agc acc ccc caa gat ggg aac gtg gtc gtc gca      433

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63 Pro Leu Ser Leu Asp Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala
64      125                      130                      135
66 tgc ctg gtc cag ggc ttc ttc ccc cag gag cca ctc agt gtg acc tgg 481
67 Cys Leu Val Gln Gly Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp
68 140                      145                      150                      155
70 agc gaa agc gga cag aac gtg acc gcc aga aac ttc cca cct agc cag 529
71 Ser Glu Ser Gly Gln Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln
72                      160                      165                      170
74 gat gcc tcc ggg gac ctg tac acc acg agc agc cag ctg acc ctg ccg 577
75 Asp Ala Ser Gly Asp Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu Pro
76                      175                      180                      185
78 gcc aca cag tgc cca gac ggc aag tcc gtg aca tgc cac gtg aag cac 625
79 Ala Thr Gln Cys Pro Asp Gly Lys Ser Val Thr Cys His Val Lys His
80                      190                      195                      200
82 tac acg aat tcc agc cag gat gtg act gtg ccc tgc cga gtt ccc cca 673
83 Tyr Thr Asn Ser Ser Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro
84      205                      210                      215
86 cct ccc cca tgc tgc cac ccc cga ctg tcg ctg cac cga ccg gcc ctc 721
87 Pro Pro Pro Cys Cys His Pro Arg Leu Ser Leu His Arg Pro Ala Leu
88 220                      225                      230                      235
90 gag gac ctg ctg tta ggt tca gaa gcg aac ctc acg tgc aca ctg acc 769
91 Glu Asp Leu Leu Leu Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr
92                      240                      245                      250
94 ggc ctg aga gat gcc tct ggt gcc acc ttc acc tgg acg ccc tca agt 817
95 Gly Leu Arg Asp Ala Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser
96                      255                      260                      265
98 ggg aag agc gct gtt caa gga cca cct gag cgt gac ctc tgt ggc tgc 865
99 Gly Lys Ser Ala Val Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys
100      270                      275                      280
102 tac agc gtg tca tca gta ctt cct ggc tgt gcc cag cca tgg aac cat 913
103 Tyr Ser Val Ser Ser Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His
104      285                      290                      295
106 ggg gag acc ttc acc tgc act gct gcc cac ccc gag ttg aag acc cca 961
107 Gly Glu Thr Phe Thr Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro
108 300                      305                      310                      315
110 cta acc gcc aac atc aca aaa tcc gga aac aca ttc cgg ccc gag gtc 1009
111 Leu Thr Ala Asn Ile Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val
112                      320                      325                      330
114 cac ctg ctg ccg ccg ccg tcg gag gag ctg gcc ctg aac gag ctg gtg 1057
115 His Leu Leu Pro Pro Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val
116                      335                      340                      345
118 acg ctg acg tgc ctg gca cgt ggc ttc agc ccc aag gat gtg ctg gtt 1105
119 Thr Leu Thr Cys Leu Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val
120                      350                      355                      360
122 cgc tgg ctg cag ggg tca cag gag ctg ccc cgc gag aag tac ctg act 1153
123 Arg Trp Leu Gln Gly Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr
124      365                      370                      375
126 tgg gca tcc cgg cag gag ccc agc cag ggc acc acc acc tat gct gtg 1201
127 Trp Ala Ser Arg Gln Glu Pro Ser Gln Gly Thr Thr Thr Tyr Ala Val

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128 380          385          390          395
130 acc agc ata ctg cgc gtg gca gcc gag gac tgg aag aag ggg gag acc 1249
131 Thr Ser Ile Leu Arg Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr
132          400          405          410
134 ttc tcc tgc atg gtg ggc cac gag gcc ctg ccg ctg gcc ttc aca cag 1297
135 Phe Ser Cys Met Val Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln
136          415          420          425
138 aag acc atc gac cgc ttg gcg ggt aaa ccc acc cat atc aat gtg tct 1345
139 Lys Thr Ile Asp Arg Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser
140          430          435          440
142 gtt gtc atg gcg gag gcg gac ggc acc tgc tac aga tgaaatattg 1391
143 Val Val Met Ala Glu Ala Asp Gly Thr Cys Tyr Arg
144          445          450          455
146 cggatccgga gggattt atg gac att gtg atg acc cag tct cca gca atc 1441
147          Met Asp Ile Val Met Thr Gln Ser Pro Ala Ile
148          460          465
150 atg tct gca tct cca ggg gag aag gtc acc ata acc tgc agt gcc agc 1489
151 Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala Ser
152          470          475          480
154 tca atg gta agt tac atg cac tgg ttc cag cag aag cca ggc act tct 1537
155 Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr Ser
156          485          490          495
158 ccc aaa ctc tgg ctt tat agc aca tcc aac ctg gct tct gga gtc cct 1585
159 Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val Pro
160          500          505          510
162 gct cgc ttc agt ggc agt gga tct ggg acc tct tac tct ctc aca atc 1633
163 Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
164 515          520          525          530
166 agc cga atg gag gct gaa gat gct gcc act tat tac tgc cat caa agg 1681
167 Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg
168          535          540          545
170 act agc tac cca tac aca ttc gga ggg ggg acc aag ctt gag atc aaa 1729
171 Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
172          550          555          560
174 cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag 1777
175 Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
176          565          570          575
178 cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac ttc 1825
179 Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
180          580          585          590
182 tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa 1873
183 Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
184 595          600          605          610
186 tcg ggt aac tcc cag gag agt gtc aca gag cag gac agc aag gac agc 1921
187 Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
188          615          620          625
190 acc tac agc ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag 1969
191 Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
192          630          635          640

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194 aaa cac aaa gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg 2017
195 Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
196          645          650          655
198 ccc gtc aca aag agc ttc aac agg gga gag tgt tgatctaga          2059
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200          660          665
203 <210> SEQ ID NO: 2
204 <211> LENGTH: 669
205 <212> TYPE: PRT
206 <213> ORGANISM: Homo sapiens
208 <400> SEQUENCE: 2
209 Met Gly Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys Pro Gly
210 1 5 10 15
212 Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
213 20 25 30
215 Tyr Asn Ile His Trp Val Lys Gln Ser Arg Gly Lys Ser Leu Glu Trp
216 35 40 45
218 Ile Gly Tyr Ile Tyr Pro Tyr Asn Gly Asn Thr Tyr Tyr Asn Gln Lys
219 50 55 60
221 Phe Lys Asn Lys Ala Thr Leu Thr Val Asp Asn Ser Ser Thr Ser Ala
222 65 70 75 80
224 Tyr Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr
225 85 90 95
227 Cys Ala Thr Tyr Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val
228 100 105 110
230 Ser Ser Ala Ser Pro Thr Ser Pro Lys Val Phe Pro Leu Ser Leu Asp
231 115 120 125
233 Ser Thr Pro Gln Asp Gly Asn Val Val Val Ala Cys Leu Val Gln Gly
234 130 135 140
236 Phe Phe Pro Gln Glu Pro Leu Ser Val Thr Trp Ser Glu Ser Gly Gln
237 145 150 155 160
239 Asn Val Thr Ala Arg Asn Phe Pro Pro Ser Gln Asp Ala Ser Gly Asp
240 165 170 175
242 Leu Tyr Thr Thr Ser Ser Gln Leu Thr Leu Pro Ala Thr Gln Cys Pro
243 180 185 190
245 Asp Gly Lys Ser Val Thr Cys His Val Lys His Tyr Thr Asn Ser Ser
246 195 200 205
248 Gln Asp Val Thr Val Pro Cys Arg Val Pro Pro Pro Pro Cys Cys
249 210 215 220
251 His Pro Arg Leu Ser Leu His Arg Pro Ala Leu Glu Asp Leu Leu Leu
252 225 230 235 240
254 Gly Ser Glu Ala Asn Leu Thr Cys Thr Leu Thr Gly Leu Arg Asp Ala
255 245 250 255
257 Ser Gly Ala Thr Phe Thr Trp Thr Pro Ser Ser Gly Lys Ser Ala Val
258 260 265 270
260 Gln Gly Pro Pro Glu Arg Asp Leu Cys Gly Cys Tyr Ser Val Ser Ser
261 275 280 285
263 Val Leu Pro Gly Cys Ala Gln Pro Trp Asn His Gly Glu Thr Phe Thr
264 290 295 300

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266 Cys Thr Ala Ala His Pro Glu Leu Lys Thr Pro Leu Thr Ala Asn Ile
267 305 310 315 320
269 Thr Lys Ser Gly Asn Thr Phe Arg Pro Glu Val His Leu Leu Pro Pro
270 325 330 335
272 Pro Ser Glu Glu Leu Ala Leu Asn Glu Leu Val Thr Leu Thr Cys Leu
273 340 345 350
275 Ala Arg Gly Phe Ser Pro Lys Asp Val Leu Val Arg Trp Leu Gln Gly
276 355 360 365
278 Ser Gln Glu Leu Pro Arg Glu Lys Tyr Leu Thr Trp Ala Ser Arg Gln
279 370 375 380
281 Glu Pro Ser Gln Gly Thr Thr Thr Tyr Ala Val Thr Ser Ile Leu Arg
282 385 390 395 400
284 Val Ala Ala Glu Asp Trp Lys Lys Gly Glu Thr Phe Ser Cys Met Val
285 405 410 415
287 Gly His Glu Ala Leu Pro Leu Ala Phe Thr Gln Lys Thr Ile Asp Arg
288 420 425 430
290 Leu Ala Gly Lys Pro Thr His Ile Asn Val Ser Val Val Met Ala Glu
291 435 440 445
293 Ala Asp Gly Thr Cys Tyr Arg Met Asp Ile Val Met Thr Gln Ser Pro
294 450 455 460
296 Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser
297 465 470 475 480
299 Ala Ser Ser Met Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly
300 485 490 495
302 Thr Ser Pro Lys Leu Trp Leu Tyr Ser Thr Ser Asn Leu Ala Ser Gly
303 500 505 510
305 Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu
306 515 520 525
308 Thr Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His
309 530 535 540
311 Gln Arg Thr Ser Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
312 545 550 555 560
314 Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser
315 565 570 575
317 Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn
318 580 585 590
320 Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala
321 595 600 605
323 Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys
324 610 615 620
326 Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp
327 625 630 635 640
329 Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu
330 645 650 655
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333 660 665
336 <210> SEQ ID NO: 3
337 <211> LENGTH: 50
338 <212> TYPE: DNA

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VERIFICATION SUMMARY

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